

ABSTRACT

Embodiments of methods are provided that can be used to estimate network relationships between genes of an organism using time course expression data and a set of linear differential equations. Aikake's Information Criterion and mask tools
5 can be used to reduce the number of elements in a matrix by determining which elements are zero or not significantly changed under the conditions of the study. Maximum likelihood estimation and new statistical methods are used to evaluate the significance of a proposed network relationship.

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